



SEQUENCE LISTING

1) GENERAL INFORMATION:

- (i) APPLICANT: Soppet, Daniel R
Yi, Li
Rosen, Craig A
Ruben, Steven
- (ii) TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
HLTDG74
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
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(C) CITY: Roseland
(D) STATE: NJ
(E) COUNTRY: USA
(F) ZIP: 07068-1739
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/468,011
(B) FILING DATE: 06-JUN-1995
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Ferraro, Gregory D
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(C) REFERENCE/DOCKET NUMBER: 325800-458
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2003 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 90..1712
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTTTGCTCTG	GGCAGCCAAG	TTGGCATATT	GGAAGCTTTT	TCCGGGCTCT	GGAGGAGGGT	60									
CCCTGCTTCT	TCCTACAGCC	GTTCCGGGC	ATG Met 1	GCC Ala	TGG Trp	CTG Leu	GGG Gly 5	GCG Ala	TCG Ser	CTC Leu	113				
CAC GTC	TGG Trp	GGT Gly	TGG Trp	CTA Leu	ATG Met 15	CTC Leu	GGC Gly	AGC Ser	TGC Cys	CTC Leu	CTG Leu	GCC Ala	AGA Arg	GCC Ala	161
CAG CTG	GAT Ser	TCT Ser	GAT Asp	GGC Gly 30	ACC Thr	ATC Ile	ACT Thr	ATA Ile	GAG Glu	GAG Glu	CAG Gln	ATT Ile	GTC Val	CTT Leu	209
GTG CTG	AAA Lys	GCG Ala	AAA Lys	GTA Val	CAA Gln	TGT Cys	GAA Glu	CTC Leu	AAC Asn	ATC Ile	ACA Thr	GCT Ala	CAA Gln	CTC Leu	257
CAG GAG	GGA Gly	GAA Glu	GGT Gly	AAT Asn	TGT Cys	TTC Phe	CCT Pro	GAA Glu	TGG Trp	GAT Asp	GGA Gly	CTC Leu	ATT Ile	TGT Cys	305
TGG CCC	AGA Arg	GGA Gly	ACA Thr	GTG Val	GGG Gly	AAA Lys	ATA Ile	TCG Ser	GCT Ala	GTT Val	CCA Pro	TGC Cys	CCT Pro	CCT Pro	353
TAT ATT	TAT Tyr	GAC Asp	TTC Phe	AAC Asn	CAT His	AAA Lys	GGA Gly	GTT Val	GCT Ala	TTC Phe	CGA Arg	CAC His	TGT Cys	AAC Asn	401
CCC AAT	GGA Gly	ACA Thr	TGG Trp	GAT Asp	TTT Phe	ATG Met	CAC His	AGC Ser	TTA Leu	AAT Asn	AAA Lys	ACA Thr	TGG Trp	GCC Ala	449
AAT TAT	TCA Ser	GAC Asp	TGC Cys	CTT Leu	CGC Arg	TTT Phe	CTG Leu	CAG Gln	CCA Pro	GAT Asp	ATC Ile	AGC Ser	ATA Ile	GGA Gly	497
AAG CAA	GAA Glu	TTC Phe	TGT Cys	GAA Glu	CGC Arg	CTC Leu	TAT Tyr	GTA Val	ATG Met	TAT Tyr	ACC Thr	GTT Val	GGC Gly	TAC Tyr	545
TCC ATC	TCT Ser	TTT Phe	GGT Gly	TCC Ser	TTG Leu	GCT Ala	GTG Val	GCT Ala	ATT Ile	CTC Leu	ATC Ile	ATT Ile	GGT Gly	TAC Tyr	593
TTC AGA	CGA Arg	TTG Leu	CAT His	TGC Cys	ACT Thr	AGG Arg	AAC Asn	TAT Tyr	ATC Ile	CAC His	ATG Met	CAC His	TTA Leu	TTT Phe	641
GTG TCT	TTC Phe	ATG Met	CTG Leu	AGA Arg	GCT Ala	ACA Thr	AGC Ser	ATC Ile	TTT Phe	GTC Val	AAA Lys	GAC Asp	AGA Arg	GTA Val	689
GTC CAT	GCT His	CAC Ala	ATA Ile	GGA Gly	GTA Val	AAG Lys	GAG Glu	CTG Leu	GAG Glu	TCC Ser	CTA Leu	ATA Ile	ATG Met	CAG Gln	737
GAT GAC	CCA Pro	CAA Gln	AAT Asn	TCC Ser	ATT Ile	GAG Glu	GCA Ala	ACT Thr	TCT Ser	GTG Val	GAC Asp	AAA Lys	TCA Ser	CAA Gln	785
TAT ATC	GGG Trp	TGC Gly	AAG Glu	ATT Ser	GCT Thr	GTT Thr	GTG Thr	ATG Thr	TTT Thr	ATT Thr	TAC Thr	TTC Thr	CTG Thr	GCT Thr	833

Tyr	Ile	Gly	Cys	Lys	Ile	Ala	Val	Val	Met	Phe	Ile	Tyr	Phe	Leu	Ala		
		235					240					245					
ACA	AAT	TAT	TAT	TGG	ATC	CTG	GTG	GAA	GGT	CTC	TAC	CTG	CAT	AAT	CTC	881	
Thr	Asn	Tyr	Tyr	Trp	Ile	Leu	Val	Glu	Gly	Leu	Tyr	Leu	His	Asn	Leu		
	250					255					260						
ATC	TTT	GTG	GCT	TTC	TTT	TCG	GAC	ACC	AAA	TAC	CTG	TGG	GGC	TTC	ATC	929	
Ile	Phe	Val	Ala	Phe	Phe	Ser	Asp	Thr	Lys	Tyr	Leu	Trp	Gly	Phe	Ile		
	265				270					275					280		
TTG	ATA	GGC	TGG	GGG	TTT	CCA	GCA	GCA	TTT	GTT	GCA	GCA	TGG	GCT	GTG	977	
Leu	Ile	Gly	Trp	Gly	Phe	Pro	Ala	Ala	Phe	Val	Ala	Ala	Trp	Ala	Val		
				285					290					295			
GCA	CGA	GCA	ACT	CTG	GCT	GAT	GCG	AGG	TGC	TGG	GAA	CTT	AGT	GCT	GGA	1025	
Ala	Arg	Ala	Thr	Leu	Ala	Asp	Ala	Arg	Cys	Trp	Glu	Leu	Ser	Ala	Gly		
			300					305					310				
GAC	ATC	AAG	TGG	ATT	TAT	CAA	GCA	CCG	ATC	TTA	GCA	GCT	ATT	GGG	CTG	1073	
Asp	Ile	Lys	Trp	Ile	Tyr	Gln	Ala	Pro	Ile	Leu	Ala	Ala	Ile	Gly	Leu		
		315					320					325					
AAT	TTT	ATT	CTG	TTT	CTG	AAT	ACG	GTT	AGA	GTT	CTA	GCT	ACC	AAA	ATC	1121	
Asn	Phe	Ile	Leu	Phe	Leu	Asn	Thr	Val	Arg	Val	Leu	Ala	Ala	Thr	Lys	Ile	
	330					335					340						
TGG	GAG	ACC	AAT	GCA	GTT	GGG	CAT	GAC	ACA	AGG	AAG	CAA	TAC	AGG	AAA	1169	
Trp	Glu	Thr	Asn	Ala	Val	Gly	His	Asp	Thr	Arg	Lys	Gln	Tyr	Arg	Lys		
	345				350					355					360		
CTG	GCC	AAA	TCG	ACA	CTG	GTC	CTG	GTC	CTA	GTC	TTT	GGA	GTG	CAT	TAC	1217	
Leu	Ala	Lys	Ser	Thr	Leu	Val	Leu	Val	Leu	Val	Phe	Gly	Val	His	Tyr		
				365					370					375			
ATC	GTG	TTC	GTG	TGC	CTG	CCT	CAC	TCC	TTC	ACT	GGG	CTC	GGG	TGG	GAG	1265	
Ile	Val	Phe	Val	Cys	Leu	Pro	His	Ser	Phe	Thr	Gly	Leu	Gly	Trp	Glu		
			380					385					390				
ATC	CGC	ATG	CAC	TGT	GAG	CTC	TTC	TTC	AAC	TCC	TTT	CAG	GGT	TTC	TTT	1313	
Ile	Arg	Met	His	Cys	Glu	Leu	Phe	Phe	Asn	Ser	Phe	Gln	Gly	Phe	Phe		
		395					400					405					
GTG	TCT	ATC	ATC	TAC	TGC	TAC	TGC	AAT	GGA	GAG	GTT	CAG	GCA	GAG	GTG	1361	
Val	Ser	Ile	Ile	Tyr	Cys	Tyr	Cys	Asn	Gly	Glu	Val	Gln	Ala	Glu	Val		
	410					415					420						
AAG	AAG	ATG	TGG	AGT	CGG	TGG	AAT	CTC	TCC	GTG	GAC	TGG	AAA	AGG	ACA	1409	
Lys	Lys	Met	Trp	Ser	Arg	Trp	Asn	Leu	Ser	Val	Asp	Trp	Lys	Arg	Thr		
	425				430					435					440		
CCG	CCA	TGT	GGC	AGC	CGC	AGA	TGC	GGC	TCA	GTG	CTC	ACC	ACC	GTG	ACG	1457	
Pro	Pro	Cys	Gly	Ser	Arg	Arg	Cys	Gly	Ser	Val	Leu	Thr	Thr	Val	Thr		
				445					450					455			
CAC	AGC	ACC	AGC	AGC	CAG	TCA	CAG	GTG	GCG	GCA	GCA	CAC	GCA	TGG	TGC	1505	
His	Ser	Thr	Ser	Ser	Gln	Ser	Gln	Val	Ala	Ala	Ala	His	Ala	Trp	Cys		
			460					465					470				
TTA	TCT	CTG	GCA	AAG	CTG	CCA	AGA	TCG	CCA	GCA	GAC	AGC	CTG	ACA	GCC	1553	
Leu	Ser	Leu	Ala	Lys	Leu	Pro	Arg	Ser	Pro	Ala	Asp	Ser	Leu	Thr	Ala		
		475					480					485					

ACA TCA UTT TAC CTG GCT ATG TCT GGA GTA ACT CAG AGC AGG ACT GCC 1601
 Thr Ser Leu Tyr Leu Ala Met Ser Gly Val Thr Gln Ser Arg Thr Ala
 490 495 500
 TCA CAC ACT CTC TCC ACG AGG AGC AAC AAG GAA GAT AGT GGG AGG CAG 1649
 Ser His Thr Leu Ser Thr Arg Ser Asn Lys Glu Asp Ser Gly Arg Gln
 505 510 515 520
 AGA GAT GAT ATT CTA ATG GAG AAG CCT TCC AGG CCT ATG GAA TCT AAC 1697
 Arg Asp Asp Ile Leu Met Glu Lys Pro Ser Arg Pro Met Glu Ser Asn
 525 530 535
 CCA GAC ACT GAA GGA TGACAAGGAG AACTGAGGA TGTCTCTGA ATGGACATGT 1752
 Pro Asp Thr Glu Gly 540
 GTGGCTGACT TTCATGGGCT GGTCCAATGG CTGGTTGTGT GAGAGGGCTT GGCTGATACT 1812
 CCTATGCTTG AGCACAAAGG CTGAAAATTC AGTTAAGGTG TTACTTAATA ATAGTTTTTA 1872
 GGCTCCATGA ATTGGCTCCT GTAAATACTA ACGACATGAA AATGCAAGTG TCAATGGAGT 1932
 AGTTTATTAC CTTCTATTGG CATCAAGTTT TCCTCTAAAT TAATGTATGG TATTTGCTCT 1992
 GTGATTGTTC A 2003

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Trp Leu Gly Ala Ser Leu His Val Trp Gly Trp Leu Met Leu
 1 5 10 15
 Gly Ser Cys Leu Leu Ala Arg Ala Gln Leu Asp Ser Asp Gly Thr Ile
 20 25 30
 Thr Ile Glu Glu Gln Ile Val Leu Val Leu Lys Ala Lys Val Gln Cys
 35 40 45
 Glu Leu Asn Ile Thr Ala Gln Leu Gln Glu Gly Glu Gly Asn Cys Phe
 50 55 60
 Pro Glu Trp Asp Gly Leu Ile Cys Trp Pro Arg Gly Thr Val Gly Lys
 65 70 75 80
 Ile Ser Ala Val Pro Cys Pro Pro Tyr Ile Tyr Asp Phe Asn His Lys
 85 90 95
 Gly Val Ala Phe Arg His Cys Asn Pro Asn Gly Thr Trp Asp Phe Met
 100 105 110
 His Ser Leu Asn Lys Thr Trp Ala Asn Tyr Ser Asp Cys Leu Arg Phe
 115 120 125
 Leu Gln Pro Asp Ile Ser Ile Gly Lys Gln Glu Phe Cys Glu Arg Leu

130

135

140

Tyr Val Met Tyr Thr Val Gly Tyr Ser Ile Ser Phe Gly Ser Leu Ala
 145 150 155 160
 Val Ala Ile Leu Ile Ile Gly Tyr Phe Arg Arg Leu His Cys Thr Arg
 165 170 175
 Asn Tyr Ile His Met His Leu Phe Val Ser Phe Met Leu Arg Ala Thr
 180 185 190
 Ser Ile Phe Val Lys Asp Arg Val Val His Ala His Ile Gly Val Lys
 195 200 205
 Glu Leu Glu Ser Leu Ile Met Gln Asp Asp Pro Gln Asn Ser Ile Glu
 210 215 220
 Ala Thr Ser Val Asp Lys Ser Gln Tyr Ile Gly Cys Lys Ile Ala Val
 225 230 235 240
 Val Met Phe Ile Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val
 245 250 255
 Glu Gly Leu Tyr Leu His Asn Leu Ile Phe Val Ala Phe Phe Ser Asp
 260 265 270
 Thr Lys Tyr Leu Trp Gly Phe Ile Leu Ile Gly Trp Gly Phe Pro Ala
 275 280 285
 Ala Phe Val Ala Ala Trp Ala Val Ala Arg Ala Thr Leu Ala Asp Ala
 290 295 300
 Arg Cys Trp Glu Leu Ser Ala Gly Asp Ile Lys Trp Ile Tyr Gln Ala
 305 310 315 320
 Pro Ile Leu Ala Ala Ile Gly Leu Asn Phe Ile Leu Phe Leu Asn Thr
 325 330 335
 Val Arg Val Leu Ala Thr Lys Ile Trp Glu Thr Asn Ala Val Gly His
 340 345 350
 Asp Thr Arg Lys Gln Tyr Arg Lys Leu Ala Lys Ser Thr Leu Val Leu
 355 360 365
 Val Leu Val Phe Gly Val His Tyr Ile Val Phe Val Cys Leu Pro His
 370 375 380
 Ser Phe Thr Gly Leu Gly Trp Glu Ile Arg Met His Cys Glu Leu Phe
 385 390 395 400
 Phe Asn Ser Phe Gln Gly Phe Phe Val Ser Ile Ile Tyr Cys Tyr Cys
 405 410 415
 Asn Gly Glu Val Gln Ala Glu Val Lys Lys Met Trp Ser Arg Trp Asn
 420 425 430
 Leu Ser Val Asp Trp Lys Arg Thr Pro Pro Cys Gly Ser Arg Arg Cys
 435 440 445
 Gly Ser Val Leu Thr Thr Val Thr His Ser Thr Ser Ser Gln Ser Gln
 450 455 460
 Val Ala Ala Ala His Ala Trp Cys Leu Ser Leu Ala Lys Leu Pro Arg

465 470 475 480
 Ser Pro Ala Asp Ser Leu Thr Ala Thr Ser Leu Tyr Leu Ala Met Ser
 485 490 495
 Gly Val Thr Gln Ser Arg Thr Ala Ser His Thr Leu Ser Thr Arg Ser
 500 505 510
 Asn Lys Glu Asp Ser Gly Arg Gln Arg Asp Asp Ile Leu Met Glu Lys
 515 520 525
 Pro Ser Arg Pro Met Glu Ser Asn Pro Asp Thr Glu Gly
 530 535 540

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAGCCGTCCC GGGCTTGGCC TGG

23

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCTCAGTGTC GACTTGTCAT CCTTCAG

27

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTTGGCATAT TGGAAGCTTT TTGCGGG

27

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAGTTTCTAG ATGTCATCCT TCAGTGTC

28

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCCTACCCGG GCCGCCATCA TGGCCTGGCT GGGGGGCCT

39

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAGTTTCTAG ATGTCATCCT TCAGTGTC

28